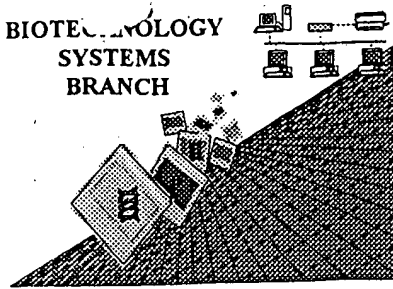O K. C...lson

p#10

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

RECEIVED

Application Serial Number: *09/445,362*

APR 2 5 2001

Source: *1653*

TECH CENTER 1600/2900

Date Processed by STIC: *4-17-01*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

RECEIVED

JUL 1 7 2001

TECH CENTER 1600/29(

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program
employing a logical and intuitive user-interface to check whether a sequence listing is in
compliance with format and content rules. Checker Version 3.0 works for sequence listings
generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old
rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual
Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-
compliant. Checker allows public users to check sequence listings in Computer Readable form
(CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence
listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> <u>SUGGESTED   CORRECTION</u>   SERIAL NUMBER: 09/445,362

RECEIVED

APR 2 5 2001

TECH CENTER 1600/2900

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid
Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ✓ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial"
(NEW RULES)

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature
(NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

SEQUENCE LISTING → Delete

<110>   MediGene Aktiengesellschaft

<120>   Myocardium- and skeletal muscle-specific nucleic acid,
its preparation and use

<150>   19725186.2
<151>   June 13, 1997

move
<170> here
to

<160>   (5) ——→   5 listed, 7 shown. See p. 4

<210> 1
<211> 1936
<212> DNA
<170> FastSEQ for Windows Version 3.0
<213> Homo sapiens

<400> 1

```
CAGCCTGCCA CTTGCCTCCC TGCCTGCTTC TGGCTGCCTT GAATGCCTGG TCCTTCAAGC    60
TCCTTCTGGG TCTGACAAAG CAGGGACCAT GTCTACCTTT GGCTACCGAA GAGGACTCAG   120
TAAATACGAA TCCATCGACG AGGATGAACT CCTCGCCTCC CTGTCAGCCG AGGAGCTGAA   180
GGAGCTAGAG AGAGAGTTGG AAGACATTGA ACCTGACCGC AACCTTCCCG TGGGGCTAAG   240
GCAAAAGAGC CTGACAGAGA AAACCCCCAC AGGGACATTC AGCAGAGAGG CACTGATGGC   300
CTATTGGGAA AAGGAGTCCC AAAAACTCTT GGAGAAGGAG AGGCTGGGGG AATGTGGAAA   360
GGTTGCAGAA GACAAAGAGG AAAGTGAAGA AGAGCTTATC TTTACTGAAA GTAACAGTGA   420
GGTTTCTGAG GAAGTGTATA CAGAGGAGGA GGAGGAGGAG TCCCAGGAGG AAGAGGAGGA   480
```

New sequence rules:
use lower case letters
for nucleic bases.

Note: See # 5 on the Error
Summary Sheet. The sequence
listing could not be processed.

<210> 3

<211> 2268   *2268 listed, 1650 shown*

<212> DNA

<213> Homo sapiens

lower case

<400> 3

```
CAGCCTGCCA CTTGCCTCCC TGCCTGCTTC TGGCTGCCTT GAATGCCTGG TCCTTCAAGC    60

TCCTTCTGGG TCTGACAAAG CAGGGACCAT GTCTACCTTT GGCTACCGAA GAGGACTCAG   120

TAAATACGAA TCCATCGACG AGGATGAACT CCTCGCCTCC CTGTCAGCCG AGGAGCTGAA   180

GGAGCTAGAG AGAGAGTTGG AAGACATTGA ACCTGACCGC AACCTTCCCG TGGGGCTAAG   240

GCAAAAGAGC CTGACAGAGA AAACCCCCAC AGGGACATTC AGCAGAGAGG CACTGATGGC   300

CTATTGGGAA AAGGAGTCCC AAAAACTCTT GGAGAAGGAG AGGCTGGGGG AATGTGGAAA   360

GGTTGCAGAA GACAAAGAGG AAAGTGAAGA AGAGCTTATC TTTACTGAAA GTAACAGTGA   420

GGTTTCTGAG GAAGTGTATA CAGAGGAGGA GGAGGAGGAG TCCCAGGAGG AAGAGGAGGA   480

AGAAGACAGT GACGAAGAGG AAAGAACAAT TGAAACTGCA AAAGGGATTA ATGGAACTGT   540

AAATTATGAT AGTGTCAATT CTGACAACTC TAAGCCAAAG ATATTTAAAA GTCAAATAGA   600

GAACATAAAT TTGACCAATG GCAGCAATGG GAGGAACACA GAGTCCCCAG CTGCCATTCA   660

CCCTTGTGGA AATCCTACAG TGATTGAGGA CGCTTTGGAC AAGATTAAAA GCAATGACCC   720

TGACACCACA GAAGTCAATT TGAACAACAT TGAGAACATC ACAACACAGA CCCTTACCCG   780

CTTTGCTGAA GCCCTCAAGG ACAACACTGT GGTGAAGACG TTCAGTCTGG CCAACACGCA   840

TGCCGACGAC AGTGCAGCCA TGGCCATTGC AGAGATGCTC AAAGCCAATG AGCACATCAC   900

CAACGTAAAC GTCGAGTCCA ACTTCATAAC GGGAAAGGGG ATCCTGGCCA TCATGAGAGC   960

TCTCCAGCAC AACACGGTGC TCACGGAGCT GCGTTTCCAT AACCAGAGGC ACATCATGGG  1020

CAGCCAGGTG GAAATGGAGA TTGTCAAGCT GCTGAAGGAG AACACGACGC TGCTGAGGCT  1080

GGGATACCAT TTTGAACTCC CAGGACCAAG AATGAGCATG ACGAGCATTT TGACAAGAAA  1140

TATGGATAAA CAGAGGCAAA AACGTTTGCA GGAGCAAAAA CAGCAGGAGG GATACGATGG  1200

AGGACCCAAT CTTAGGACCA AAGTCTGGCA AAGAGGAACA CCTAGCTCTT CACCTTATGT  1260

ATCTCCCAGG CACTCACCCT GGTCATCCCC AAAACTCCCC AAAAAAGTCC AGACTGTGAG  1320

GAGCCGTCCT CTGTCTCCTG TGGCCACACT TCCTCCTCCT CCCCCTCCTC CTCCTCCTCC  1380

CCCTCCTTCT TCCCAAAGGC TGCCACCACC TCCTCCTCCT CCCCCTCCTC CACTCCCAGA  1440

GAAAAAGCTC ATTACCAGAA ACATTGCAGA AGTCATCAAA CAACAGGAGA GTGCCCAACG  1500

GGCATTACAA AATGGACAAA AAAGAAAAA AGGGAAAAAG GTCAAGAAAC AGCCAAACAG  1560

TATTCTAAAG GAAATAAAAA ATTCTCTGAG GTCAGTGCAA GAGAAGAAAA TGGAAGACAG  1620

TTCCCGACCT TCTACCCCAC AGAGATCAGC(¥Á□q□□□□□□□□¿□□□□□□□□□□□□□□□□p□□ )
```

(1650)   *Delete non-ascii garbage.*

□□□□□□□□□□□□□□□

□□²□□□□□□□
□□□□□□t
□□□□□□□ïïoÎ§À□ì□

□□□□□□ì□□□□□□□u□□

□□□
□□□□□□□□SEQUE

NCE LISTING

← Non-ascii garbage throughout the middle of the sequence listing. See #5 on the Error Summary Sheet.

<110> MediGene Aktiengesellschaft

<120> Myocardium-

nd skeletal muscle-specific nucleic acid, its preparation and use

<150> 19725186.2
<151>

June 13, 1997

<160> 5

Sequence listing appears to begin again.

<400> 7

Pro Thr Arg Asn Pro Thr Thr Val Gln Pro Trp Ser Leu Gln Arg Cys

1   5   10   15

Ile Lys Val Asn Glu His Ile Thr Asn Val Asn Val Glu Ser Asn Phe

          20   25   30

Ile Thr Gly Lys Gly Ile Leu Ala Ile Met Arg Ala Leu Gln His Asn

          35   40   45

Thr Val Leu Thr Glu Leu Arg Phe His Asn Gln Arg His Ile Met Gly

     50   55   60

Ser Gln Val Glu Met Glu Ile Val Lys Leu Leu Lys Glu Asn Thr Thr

65   70   75   80

Leu Leu Arg Leu Gly Tyr His Phe Lys Leu Pro Gly

          85   90